

# Nathan Wemmer

Code ▼

This is an R Markdown (<http://rmarkdown.rstudio.com>) Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

## Chapter 8

### Section 8.1

#### Section 8.1.1

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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Hide

```
data <- read.table("das.txt",header=T)
names(data)
```

```
[1] "y"
```

Hide

```
attach(data)
```

The following object is masked `_by_ .GlobalEnv`:

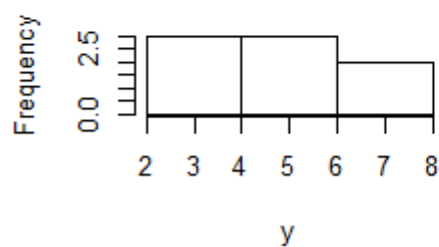
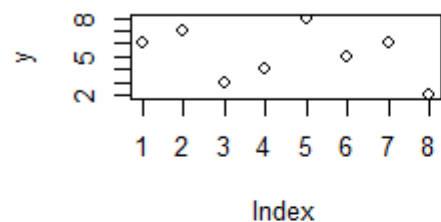
```
y
```

Hide

```
par(mfrow=c(2,2))
plot(y)
boxplot(y)
```

Hide

```
hist(y,main="")
y2 <- y
y2[52] <- 21.75
plot(y2)
```



Hide

```
summary(y)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
2.000	3.750	5.500	5.125	6.250	8.000

Hide

```
fivenum(y)
```

```
[1] 2.0 3.5 5.5 6.5 8.0
```

Hide

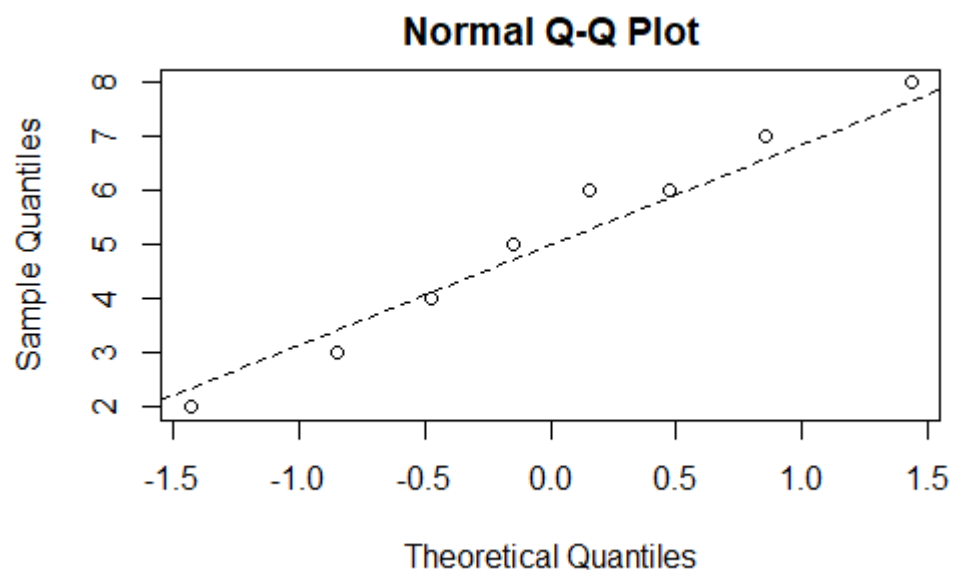
```
x <- sort(y)
n <- length(y)
d <- c(1, 0.5 * floor(0.5 * (n + 3)), 0.5 * (n + 1), n + 1 - 0.5 *
      floor(0.5 * (n + 3)), n)
0.5 * (x[floor(d)] + x[ceiling(d)])
```

```
[1] 2.0 3.5 5.5 6.5 8.0
```

## Section 8.1.2

[Hide](#)

```
par(mfrow=c(1,1))  
qqnorm(y)  
qqline(y,lty=2)
```

[Hide](#)

```
NA  
NA
```

## Section 8.1.3

[Hide](#)

```
x <- exp(rnorm(30))  
shapiro.test(x)
```

Shapiro-Wilk normality test

```
data: x  
W = 0.71808, p-value = 2.891e-06
```

## Section 8.1.4

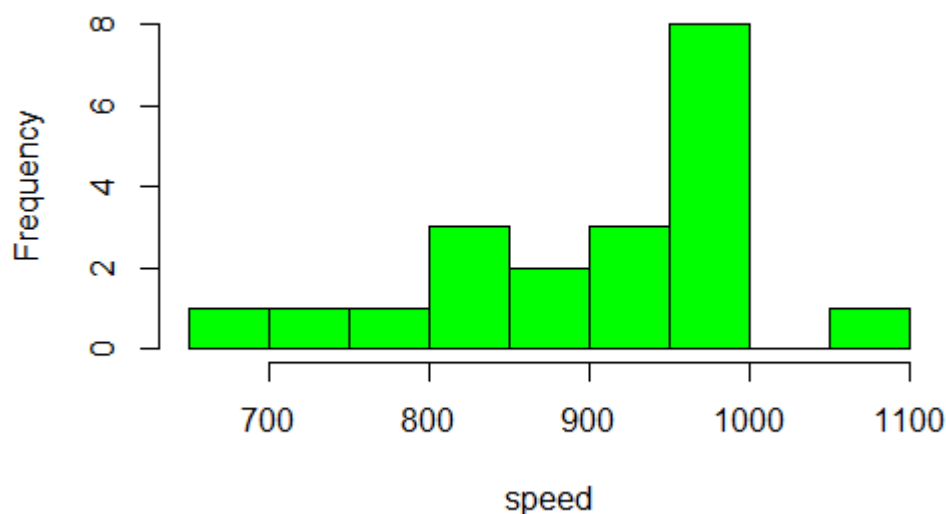
Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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Hide

```
light <- read.table("light.txt",header=T)
attach(light)
hist(speed,main="",col="green")
```



Hide

```
summary(speed)
```

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
650	850	940	909	980	1070

Hide

```
wilcox.test(speed,mu=990)
```

```
cannot compute exact p-value with ties
```

Wilcoxon signed rank test with continuity correction

data: speed

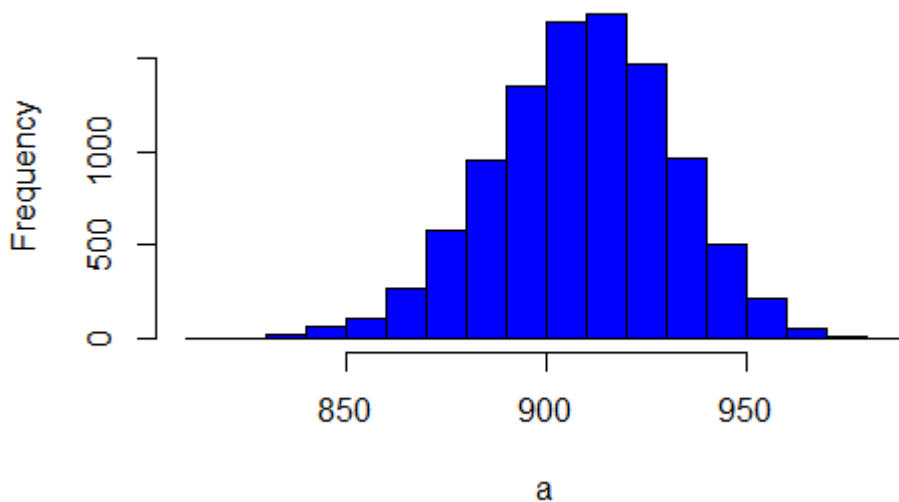
V = 22.5, p-value = 0.00213

alternative hypothesis: true location is not equal to 990

## Section 8.2

[Hide](#)

```
a <- numeric(10000)
for(i in 1:10000) a[i] <- mean(sample(speed,replace=T))
hist(a,main="",col="blue")
```



## Section 8.3

### Section 8.3.1

[Hide](#)

```
windows(7,4)
par(mfrow=c(1,2))
x <- seq(0,4,0.01)
plot(x,dgamma(x,2,2),type="l",ylab="f(x)",xlab="x",col="red")

text(2.7,0.5,"positive skew")
```

[Hide](#)

```
plot(4-x,dgamma(x,2,2),type="l",ylab="f(x)",xlab="x",col="red")
text(1.3,0.5,"negative skew")
```

Hide

```
skew <- function(x){
  m3 <- sum((x-mean(x))^3)/length(x)
  s3 <- sqrt(var(x))^3
  m3/s3
}

# data <- read.table("c:\\temp\\skewdata.txt",header=T)
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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Hide

```
data <- read.table("skewdata.txt",header=T)
attach(data)
names(data)
```

```
[1] "values"
```

Hide

```
hist(values)
skew(values)
```

```
[1] 1.318905
```

Hide

```
skew(values)/sqrt(6/length(values))
```

```
[1] 2.949161
```

Hide

```
1-pt(2.949,28)
```

```
[1] 0.003185136
```

Hide

```
skew(sqrt(values))/sqrt(6/length(values))
```

```
[1] 1.474851
```

[Hide](#)

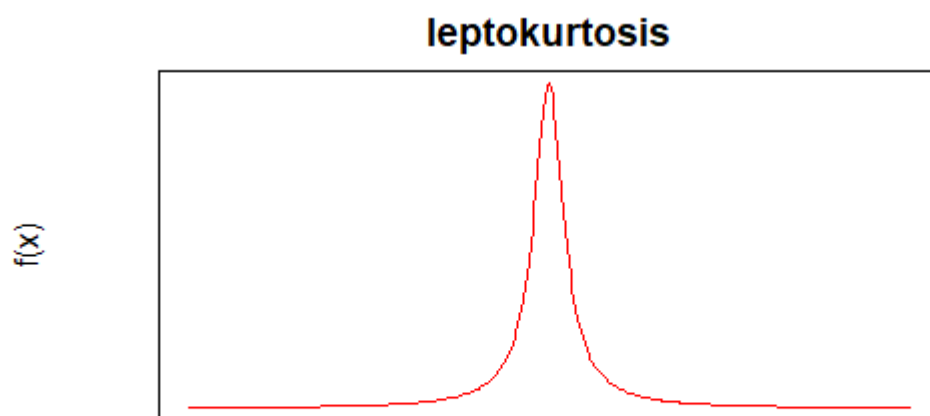
```
skew(log(values))/sqrt(6/length(values))
```

```
[1] -0.6600605
```

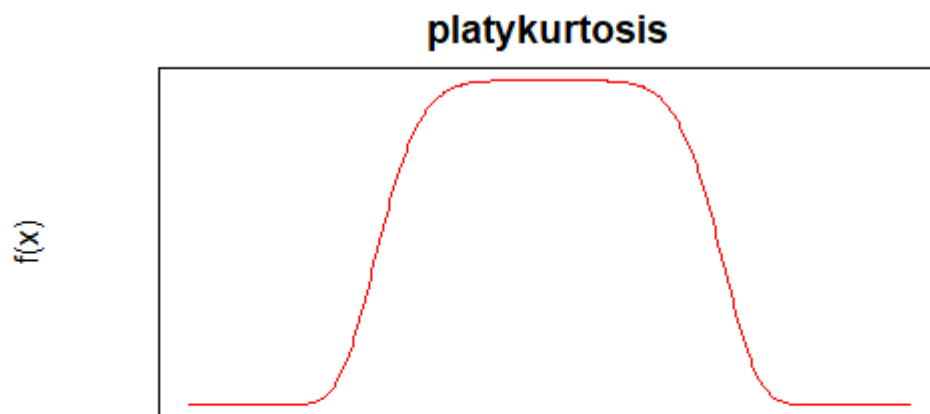
## Section 8.3.2

[Hide](#)

```
plot(-200:200,dcauchy(-200:200,0,10),type="l",ylab="f(x)",xlab="",yaxt="n",  
     xaxt="n",main="leptokurtosis",col="red")
```

[Hide](#)

```
xv <- seq(-2,2,0.01)  
plot(xv,exp(-abs(xv)^6),type="l",ylab="f(x)",xlab="",yaxt="n",  
     xaxt="n",main="platykurtosis",col="red")
```

[Hide](#)

```
kurtosis <- function(x) {  
  m4 <- sum((x-mean(x))^4)/length(x)  
  s4 <- var(x)^2  
  m4/s4 - 3 }  
  
kurtosis(values)
```

```
[1] 1.297751
```

[Hide](#)

```
kurtosis(values)/sqrt(24/length(values))
```

```
[1] 1.45093
```

## Section 8.4

### Section 8.4.1

[Hide](#)

```
qf(0.975,9,9)
```

```
[1] 4.025994
```

[Hide](#)



```
#f.test.data <- read.table("c:\\temp\\f.test.data.txt",header = T)
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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[Hide](#)

```
f.test.data <- read.table("f.test.data.txt",header = T)

attach(f.test.data)
names(f.test.data)
```

```
[1] "gardenB" "gardenC"
```

[Hide](#)

```
var(gardenB)
```

```
[1] 1.333333
```

[Hide](#)

```
var(gardenC)
```

```
[1] 14.22222
```

[Hide](#)

```
F.ratio <- var(gardenC)/var(gardenB)
F.ratio
```

```
[1] 10.66667
```

[Hide](#)

```
2*(1-pf(F.ratio,9,9))
```

```
[1] 0.001624199
```

[Hide](#)

```
var.test(gardenB,gardenC)
```

F test to compare two variances

data: gardenB and gardenC

F = 0.09375, num df = 9, denom df = 9, p-value = 0.001624

alternative hypothesis: true ratio of variances is not equal to 1

95 percent confidence interval:

0.02328617 0.37743695

sample estimates:

ratio of variances

0.09375

[Hide](#)

```
#refs <- read.table("c:\\temp\\refuge.txt",header=T)
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
refs <- read.table("refuge.txt",header=T)
```

```
attach(refs)
```

The following object is masked from package:base:

T

[Hide](#)

```
names(refs)
```

```
[1] "B" "T"
```

[Hide](#)

```
tapply(B,T,var)
```

1	2	3	4	5	6
1354.024	2025.431	3125.292	1077.030	2542.599	2221.982
7	8	9			
1445.490	1459.955	NA			

[Hide](#)

```
which(T==9)
```

```
[1] 31
```

[Hide](#)

```
bartlett.test(B[-31],T[-31])
```

## Bartlett test of homogeneity of variances

data: B[-31] and T[-31]

Bartlett's K-squared = 13.199, df = 7, p-value = 0.06741

[Hide](#)

```
fligner.test(B[-31],T[-31])
```

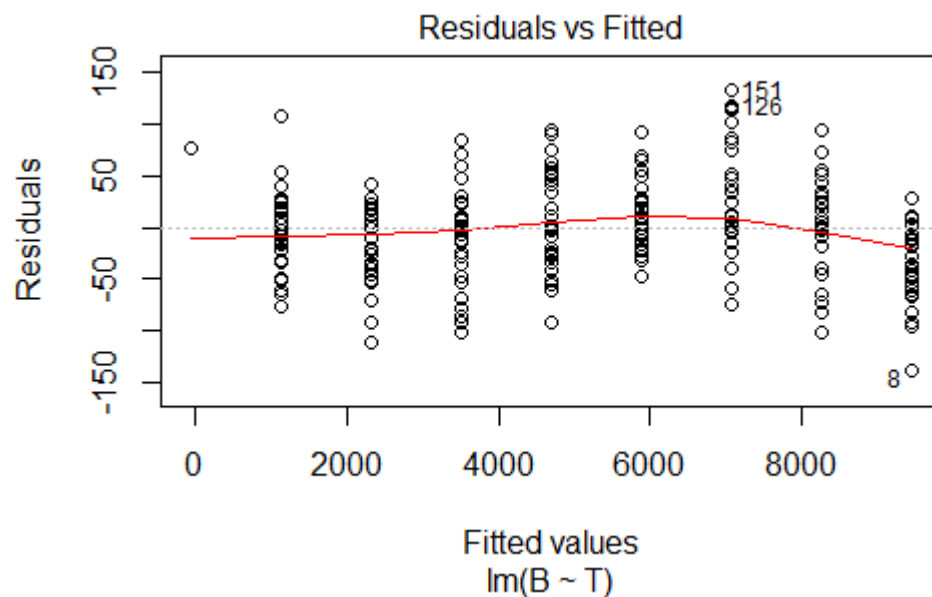
## Fligner-Killeen test of homogeneity of variances

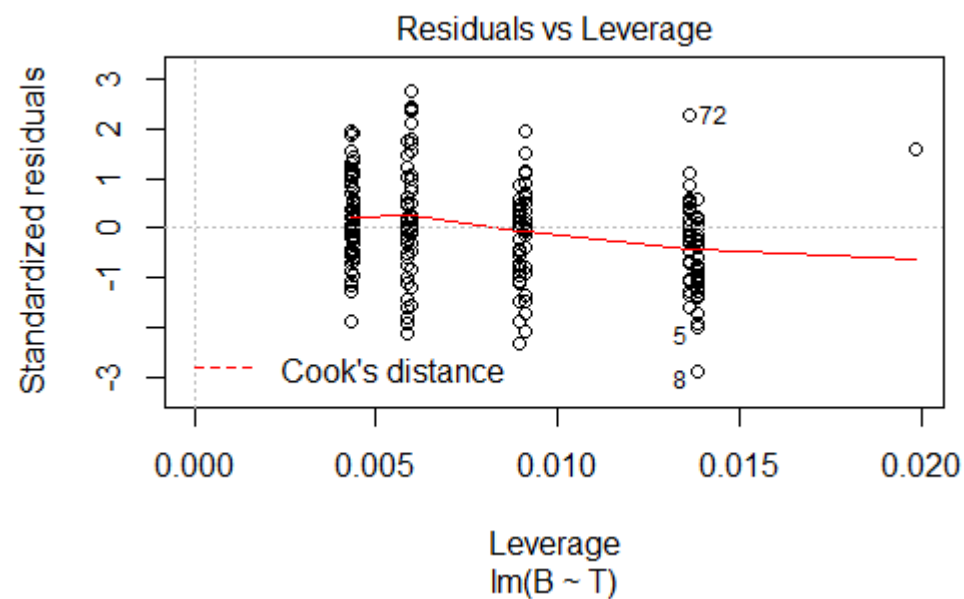
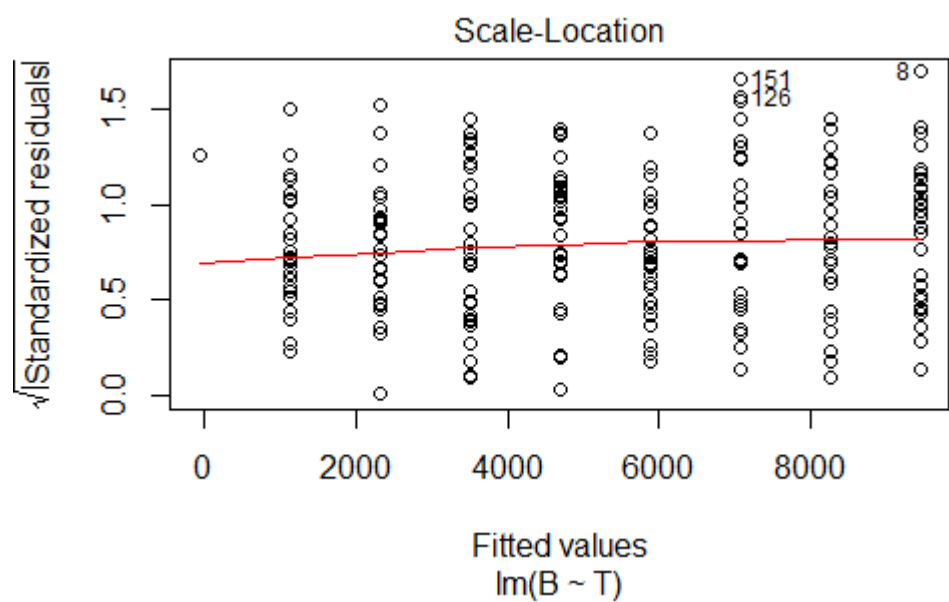
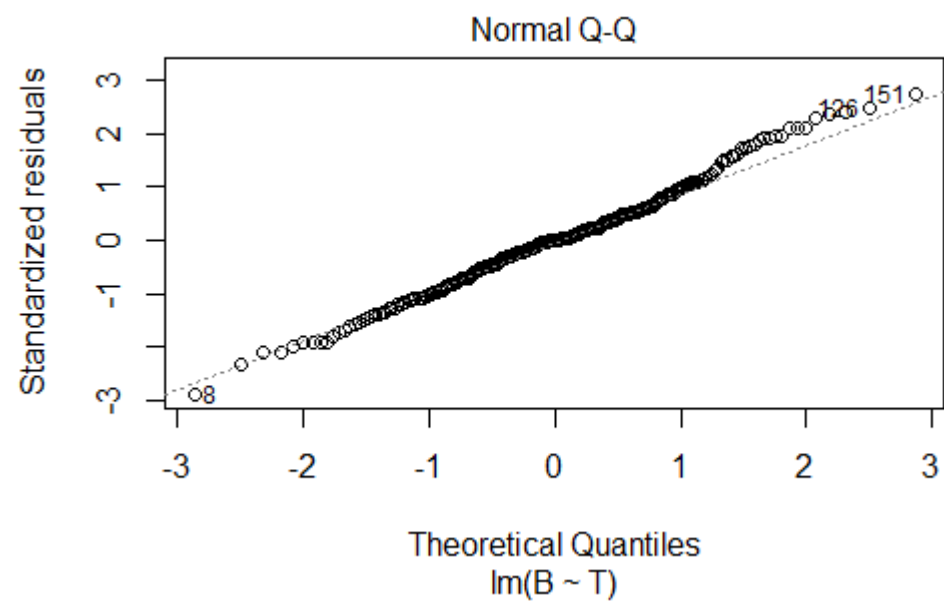
data: B[-31] and T[-31]

Fligner-Killeen:med chi-squared = 14.386, df = 7, p-value = 0.04472

[Hide](#)

```
model <- lm(B~T)
plot(model)
```





Hide

```
#ozone <- read.table("c:\\temp\\gardens.txt",header=T)
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
ozone <- read.table("gardens.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

Hide

```
attach(ozone)
```

The following objects are masked from f.test.data:

gardenB, gardenC

Hide

```
names(ozone)
```

```
[1] "gardenA" "gardenB" "gardenC"
```

Hide

```
y <- c(gardenA,gardenB,gardenC)
garden <- factor(rep(c("A","B","C"),c(10,10,10)))
var.test(gardenB,gardenC)
```

F test to compare two variances

data: gardenB and gardenC

F = 0.09375, num df = 9, denom df = 9, p-value =  
0.001624

alternative hypothesis: true ratio of variances is not equal to 1

95 percent confidence interval:

0.02328617 0.37743695

sample estimates:

ratio of variances

0.09375

Hide

```
fligner.test(y~garden)
```

Fligner-Killeen test of homogeneity of variances

data: y by garden

Fligner-Killeen:med chi-squared = 1.8061, df = 2,  
p-value = 0.4053

## Section 8.4.2

## Section 8.4.3

[Hide](#)

```
qt(0.975,18)
```

```
[1] 2.100922
```

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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[Hide](#)

```
#t.test.data <- read.table("c:\\temp\\t.test.data.txt",header=T)
t.test.data <- read.table("t.test.data.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

[Hide](#)

```
attach(t.test.data)
```

The following objects are masked from ozone:

gardenA, gardenB

The following object is masked from f.test.data:

gardenB

[Hide](#)

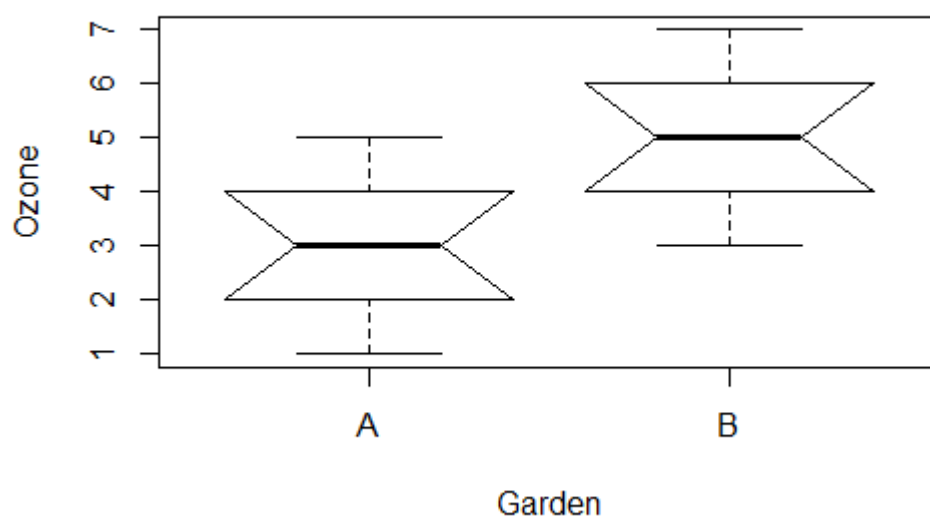
```
par(mfrow=c(1,1))
names(t.test.data)
```

```
[1] "gardenA" "gardenB"
```

[Hide](#)

```
ozone <- c(gardenA,gardenB)
label <- factor(c(rep("A",10),rep("B",10)))
boxplot(ozone~label,notch=T,xlab="Garden",ylab="Ozone")
```

the condition has length > 1 and only the first element will be used

[Hide](#)

```
s2A <- var(gardenA)
s2B <- var(gardenB)

(mean(gardenA)-mean(gardenB))/sqrt(s2A/10+s2B/10)
```

```
[1] -3.872983
```

[Hide](#)

```
2*pt(-3.872983,18)
```

```
[1] 0.00111454
```

[Hide](#)

```
t.test(gardenA,gardenB)
```

## Welch Two Sample t-test

```
data: gardenA and gardenB
t = -3.873, df = 18, p-value = 0.001115
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -3.0849115 -0.9150885
sample estimates:
mean of x mean of y
      3      5
```

Hide

```
# 8.4.4 Wilcoxon rank-sum test
ozone <- c(gardenA,gardenB)
ozone
```

```
[1] 3 4 4 3 2 3 1 3 5 2 5 5 6 7 4 4 3 5 6 5
```

Hide

```
label <- c(rep("A",10),rep("B",10))
label
```

```
[1] "A" "A" "A" "A" "A" "A" "A" "A" "A" "A" "B" "B" "B" "B"
[15] "B" "B" "B" "B" "B" "B"
```

Hide

```
combined.ranks <- rank(ozone)
combined.ranks
```

```
[1] 6.0 10.5 10.5 6.0 2.5 6.0 1.0 6.0 15.0 2.5 15.0
[12] 15.0 18.5 20.0 10.5 10.5 6.0 15.0 18.5 15.0
```

Hide

```
tapply(combined.ranks,label,sum)
```

```
 A   B
66 144
```

Hide

```
wilcox.test(gardenA,gardenB)
```

```
cannot compute exact p-value with ties
```



Wilcoxon rank sum test with continuity correction

data: gardenA and gardenB

W = 11, p-value = 0.002988

alternative hypothesis: true location shift is not equal to 0

## Section 8.5

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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[Hide](#)

```
streams <- read.table("streams.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

[Hide](#)

```
attach(streams)  
names(streams)
```

```
[1] "down" "up"
```

[Hide](#)

```
t.test(down,up)
```

Welch Two Sample t-test

data: down and up

t = -0.40876, df = 29.755, p-value = 0.6856

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-5.248256 3.498256

sample estimates:

mean of x mean of y

12.500 13.375

Hide

```
t.test(down,up,paired=TRUE)
```

#### Paired t-test

```
data: down and up
t = -3.0502, df = 15, p-value = 0.0081
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.4864388 -0.2635612
sample estimates:
mean of the differences
      -0.875
```

Hide

```
difference <- up - down
t.test(difference)
```

#### One Sample t-test

```
data: difference
t = 3.0502, df = 15, p-value = 0.0081
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.2635612 1.4864388
sample estimates:
mean of x
    0.875
```

## Section 8.6

Hide

```
sign.test <- function(x, y)
{
  if(length(x) != length(y)) stop("The two variables must be the same length")
  d <- x - y
  binom.test(sum(d > 0), length(d))
}

sign.test(gardenA,gardenB)
```

Exact binomial test

```
data:  sum(d > 0) and length(d)
number of successes = 0, number of trials = 10,
p-value = 0.001953
alternative hypothesis: true probability of success is not equal to 0.5
95 percent confidence interval:
 0.0000000 0.3084971
sample estimates:
probability of success
      0
```

## Section 8.7

[Hide](#)

```
prop.test(c(4,196),c(40,3270))
```

Chi-squared approximation may be incorrect

2-sample test for equality of proportions with continuity correction

```
data:  c(4, 196) out of c(40, 3270)
X-squared = 0.52289, df = 1, p-value = 0.4696
alternative hypothesis: two.sided
95 percent confidence interval:
 -0.06591631  0.14603864
sample estimates:
   prop 1    prop 2 
0.1000000 0.05993884
```

## Section 8.8

### Section 8.8.1

[Hide](#)

```
qchisq(0.95,1)
```

```
[1] 3.841459
```

[Hide](#)

```
count <- matrix(c(38,14,11,51),nrow=2)
count
```

```
      [,1] [,2]
[1,]   38   11
[2,]   14   51
```

Hide

```
chisq.test(count)
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: count
X-squared = 33.112, df = 1, p-value = 8.7e-09
```

Hide

```
chisq.test(count,correct=F)
```

Pearson's Chi-squared test

```
data: count
X-squared = 35.334, df = 1, p-value = 2.778e-09
```

Hide

```
chisq.test(count,correct=F)$expected
```

```
      [,1]      [,2]
[1,] 22.35088 26.64912
[2,] 29.64912 35.35088
```

## Section 8.8.2

## Section 8.8.3

Hide

```
chisq.test(c(10,3,2,6))
```

Chi-squared test for given probabilities

```
data:  c(10, 3, 2, 6)
X-squared = 7.381, df = 3, p-value = 0.0607
```

[Hide](#)

```
chisq.test(c(10,3,2,6),p=c(0.2,0.2,0.3,0.3))
```

Chi-squared approximation may be incorrect

Chi-squared test for given probabilities

```
data:  c(10, 3, 2, 6)
X-squared = 11.302, df = 3, p-value = 0.0102
```

## Section 8.8.4

[Hide](#)

```
die <- ceiling(runif(100,0,6))
table(die)
```

```
die
 1  2  3  4  5  6
24  9 17 15 16 19
```

[Hide](#)

```
chisq.test(table(die))
```

Chi-squared test for given probabilities

```
data:  table(die)
X-squared = 7.28, df = 5, p-value = 0.2006
```

## Section 8.8.5

[Hide](#)

```
factorial(8)*factorial(12)*factorial(10)*factorial(10)/
(factorial(6)*factorial(2)*factorial(4)*factorial(8)*factorial(20))
```

```
[1] 0.07501786
```

[Hide](#)

```
factorial(8)*factorial(12)*factorial(10)*factorial(10)/  
(factorial(7)*factorial(3)*factorial(1)*factorial(9)*factorial(20))
```

```
[1] 0.009526078
```

[Hide](#)

```
factorial(8)*factorial(12)*factorial(10)*factorial(10)/  
(factorial(8)*factorial(2)*factorial(0)*factorial(10)*factorial(20))
```

```
[1] 0.0003572279
```

[Hide](#)

```
0.07501786 + 0.009526078 + 0.000352279
```

```
[1] 0.08489622
```

[Hide](#)

```
2*(0.07501786 + 0.009526078 + 0.000352279)
```

```
[1] 0.1697924
```

[Hide](#)

```
x <- as.matrix(c(6,4,2,8))  
dim(x) <- c(2,2)  
x
```

```
      [,1] [,2]  
[1,]    6    2  
[2,]    4    8
```

[Hide](#)

```
fisher.test(x)
```

## Fisher's Exact Test for Count Data

```
data:  x
p-value = 0.1698
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
  0.6026805 79.8309210
sample estimates:
odds ratio
  5.430473
```

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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Hide

```
#table <- read.table("c:\\temp\\fisher.txt",header=TRUE)
table <- read.table("fisher.txt",header=TRUE)

head(table)
```

	<b>tree</b> <fctr>	<b>nests</b> <fctr>
1	A	ants
2	B	ants
3	A	none
4	A	ants
5	B	none
6	A	none

6 rows

Hide

```
attach(table)
fisher.test(tree,nests)
```

## Fisher's Exact Test for Count Data

```
data: tree and nests
p-value = 0.1698
alternative hypothesis: true odds ratio is not equal to 1
95 percent confidence interval:
 0.6026805 79.8309210
sample estimates:
odds ratio
 5.430473
```

## Section 8.9

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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Hide

```
data <- read.table("twosample.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

Hide

```
attach(data)
```

The following objects are masked \_by\_ .GlobalEnv:

a, x, y

The following object is masked from data (pos = 11):

y

Hide

```
plot(xx,yy,pch=21,col="red",bg="orange")
```

```
Error in plot(xx, yy, pch = 21, col = "red", bg = "orange") :
  object 'xx' not found
```



## Section 8.9.1

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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Hide

```
pollute <- read.table("Pollute.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

Hide

```
attach(pollute)
cor(pollute)
```

	Pollution	Temp	Industry	Population
Pollution	1.00000000	-0.43360020	0.64516550	0.49377958
Temp	-0.43360020	1.00000000	-0.18788200	-0.06267813
Industry	0.64516550	-0.18788200	1.00000000	0.95545769
Population	0.49377958	-0.06267813	0.95545769	1.00000000
Wind	0.09509921	-0.35112340	0.23650590	0.21177156
Rain	0.05428389	0.38628047	-0.03121727	-0.02606884
Wet.days	0.36956363	-0.43024212	0.13073780	0.04208319
	Wind	Rain	Wet.days	
Pollution	0.09509921	0.05428389	0.36956363	
Temp	-0.35112340	0.38628047	-0.43024212	
Industry	0.23650590	-0.03121727	0.13073780	
Population	0.21177156	-0.02606884	0.04208319	
Wind	1.00000000	-0.01246601	0.16694974	
Rain	-0.01246601	1.00000000	0.49605834	
Wet.days	0.16694974	0.49605834	1.00000000	

Hide

```
cor(Pollution,Wet.days)
```

```
[1] 0.3695636
```

## Section 8.9.2

# Section 8.9.3 skip

# Section 8.9.4

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/school/statistical data management/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
productivity <- read.table("productivity.txt",header=T)
```

the condition has length > 1 and only the first element will be usedthe condition has length > 1 and only the first element will be used

Hide

```
attach(productivity)
```

The following objects are masked `_by_ .GlobalEnv:`

    x, y

The following objects are masked from data (pos = 4):

    x, y

The following object is masked from data (pos = 13):

    y

Hide

```
head(productivity)
```

	x	y	f
	<int>	<int>	<fctr>
1	1	3	a
2	2	4	a
3	3	2	a
4	4	1	a

	x <int>	y f <int> <fctr>
5	5	3 a
6	6	1 a
6 rows		

[Hide](#)

```
plot(x,y,pch=21,col="blue",bg="green",  
      xlab="Productivity",ylab="Mammal species")
```

```
Error in xy.coords(x, y, xlabel, ylabel, log) :  
  'x' and 'y' lengths differ
```

## Section 8.10 skip

## Section 8.11

[Hide](#)

```
power.t.test(delta=2,sd=3.5,power=0.8)
```

Two-sample t test power calculation

```
      n = 49.05349  
delta = 2  
    sd = 3.5  
sig.level = 0.05  
  power = 0.8  
alternative = two.sided
```

NOTE: n is number in *each* group

[Hide](#)

```
power.t.test(n=15,sd=3.5,power=0.8)
```

Two-sample t test power calculation

```
n = 15
delta = 3.709303
sd = 3.5
sig.level = 0.05
power = 0.8
alternative = two.sided
```

NOTE: n is number in *each* group

## Section 8.12

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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[Hide](#)

```
data <- read.table("skewdata.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

[Hide](#)

```
attach(data)
```

The following object is masked from data (pos = 12):

```
values
```

[Hide](#)

```
names(data)
```

```
[1] "values"
```

[Hide](#)

```
ms <- numeric(10000)
for (i in 1:10000){
  ms[i] <- mean(sample(values, length(values),replace=TRUE, prob=NULL)) }

quantile(ms,c(0.025,0.975))
```

```
      2.5%      97.5%
24.92025 37.80850
```

Hide

```
mean(values)-quantile(ms,c(0.025,0.975))
```

```
      2.5%      97.5%
6.048403 -6.839841
```

Hide

```
1.96*sqrt(var(values)/length(values))
```

```
[1] 6.569802
```

Hide

```
install.packages("boot")
```

WARNING: Rtools is required to build R packages but is not currently installed. Please download and install the appropriate version of Rtools before proceeding:

```
https://cran.rstudio.com/bin/windows/Rtools/
Installing package into 勔牻C:/Users/Nathan/Documents/R/win-library/3.6勔牻
(as 勔牻lib勔牻 is unspecified)
trying URL 'https://cran.rstudio.com/bin/windows/contrib/3.6/boot_1.3-23.zip'
Content type 'application/zip' length 639896 bytes (624 KB)
downloaded 624 KB
```

package 'boot' successfully unpacked and MD5 sums checked

The downloaded binary packages are in  
C:\Users\Nathan\AppData\Local\Temp\Rtmp0E09Fm\downloaded\_packages

Hide

```
library(boot)

mymean <- function(values,i) mean(values[i])

myboot <- boot(values,mymean,R=10000)
myboot
```

## ORDINARY NONPARAMETRIC BOOTSTRAP

Call:

```
boot(data = values, statistic = mymean, R = 10000)
```

Bootstrap Statistics :

	original	bias	std. error
t1*	30.96866	0.02697891	3.31953

Hide

```
mean(values)
```

```
[1] 30.96866
```

Hide

```
mean(myboot$t)-mean(values)
```

```
[1] 0.02697891
```

Hide

```
sqrt(var(myboot$t))
```

```
      [,1]
[1,] 3.31953
```

Hide

```
windows(7,4)
par(mfrow=c(2,1))
hist(ms)
hist(myboot$t)
```

Hide

```
mean(values)-quantile(myboot$t,c(0.025,0.975))
```

	2.5%	97.5%
	5.996037	-6.925040

Hide

```
boot.ci(myboot)
```

bootstrap variances needed for studentized intervals

#### BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS

Based on 10000 bootstrap replicates

CALL :

```
boot.ci(boot.out = myboot)
```

Intervals :

Level	Normal	Basic
95%	(24.44, 37.45 )	(24.04, 36.98 )

Level	Percentile	BCa
95%	(24.95, 37.90 )	(25.53, 38.84 )

Calculations and Intervals on Original Scale

Hide

```
quantile(myboot$t,c(0.025,0.975))
```

2.5%	97.5%
24.97262	37.89370

## END OF CHAPTER 8

## Chapter 9

### Section 9.1

### Section 9.2

### Section 9.3

### Section 9.4

### Section 9.5

### Section 9.6

### Section 9.6.2

Hide

```
xnames <- paste("x", 1:25, sep="")
(model.formula <- as.formula(paste("y~", paste(xnames, collapse= "+"))))
```

```
y ~ x1 + x2 + x3 + x4 + x5 + x6 + x7 + x8 + x9 + x10 + x11 +
    x12 + x13 + x14 + x15 + x16 + x17 + x18 + x19 + x20 + x21 +
    x22 + x23 + x24 + x25
```

## Section 9.7

Hide

```
A <- rep(1:2,each=12)
B <- rep(1:4,each=3,length=24)
C <- rep(1:3,length=24)

a <- factor(A)
b <- factor(A):factor(B)
c <- factor(A):factor(B):factor(C)
```

## Section 9.8

## Section 9.9

## Section 9.10

Hide

```
windows(7,4)
par(mfrow=c(1,2))
x <- seq(0,10,0.1)
plot(x,1+x-x^2/15,type="l",col="red")
plot(x,3+0.1*exp(x),type="l",col="red")
```

## Section 9.11

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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Hide

```
data <- read.delim("timber.txt")
attach(data)
```

The following objects are masked from data (pos = 4):

girth, height, volume

Hide

```
names(data)
```

```
[1] "volume" "girth"  "height"
```

Hide

```
library(MASS)

windows(7,7)
boxcox(volume~log(girth)+log(height))
boxcox(volume~log(girth)+log(height),lambda=seq(-0.5,0.5,0.01))
```

Hide

```
boxcox(volume~girth+height)
boxcox(volume~girth+height,lambda=seq(0.1,0.6,0.01))
```

## Section 9.12

## Section 9.13

## Section 9.13.2

Hide

```
mcheck <- function (obj, ...){
  rs <- obj$resid
  fv <- obj$fitted
  windows(7,4)
  par(mfrow=c(1,2))
  plot(fv,rs,xlab="Fitted values",ylab="Residuals",pch=16,col="red")
  abline(h=0, lty=2)
  qqnorm(rs,xlab="Normal scores",ylab="Ordered residuals",main="",pch=16)
  qqline(rs,lty=2,col="green")
  par(mfrow=c(1,1))
  invisible(NULL) }

# Normal errors

x <- 0:30
e <- rnorm(31,mean=0,sd=5)
yn <- 10+x+e
mn <- lm(yn~x)
mcheck(mn)

# Uniform errors
eu <- 20*(runif(31)-0.5)
yu <- 10+x+eu
mu <- lm(yu~x)
mcheck(mu)
```

[Hide](#)

```
# Negative binomial errors
enb <- rnbinom(31,2,.3)
ynb <- 10+x+enb
mnb <- lm(ynb~x)
mcheck(mnb)

# Gamma errors and increasing variance

eg <- rgamma(31,1,1/x)
yg <- 10+x+eg
mg <- lm(yg~x)
mcheck(mg)
```

[Hide](#)

## Section 9.14

```
x <- c(2,3,3,3,4)
y <- c(2,3,2,1,2)

windows(7,4)
par(mfrow=c(1,2))
plot(x,y,xlim=c(0,8),ylim=c(0,8))

x1 <- c(x,7)
y1 <- c(y,6)
plot(x1,y1,xlim=c(0,8),ylim=c(0,8))
```

Hide

```
abline(lm(y1~x1),col="blue")

reg <- lm(y1~x1)
summary(reg)
```

```
Call:
lm(formula = y1 ~ x1)

Residuals:
    1      2      3      4      5      6 
0.78261 0.91304 -0.08696 -1.08696 -0.95652 0.43478 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -0.5217     0.9876  -0.528   0.6253
x1             0.8696     0.2469   3.522   0.0244 *
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9668 on 4 degrees of freedom
Multiple R-squared:  0.7561,    Adjusted R-squared:  0.6952 
F-statistic: 12.4 on 1 and 4 DF,  p-value: 0.02441
```

Hide

```
influence.measures(reg)
```

```
Influence measures of
lm(formula = y1 ~ x1) :
```

	dfb.1_ <dbl>	dfb.x1 <dbl>	dffit <dbl>	cov.r <dbl>	cook.d <dbl>	hat inf <dbl> <fctr>
1	0.6872847	-0.5286805	0.73256123	1.5285825	0.267906977	0.3478261
2	0.3817691	-0.2036102	0.52899479	1.1547525	0.134846349	0.1956522

	<b>dfb.1_</b> <dbl>	<b>dfb.x1</b> <dbl>	<b>dffit</b> <dbl>	<b>cov.r</b> <dbl>	<b>cook.d</b> <dbl>	<b>hat inf</b> <dbl> <fctr>
3	-0.0309508	0.0165071	-0.04288669	2.1991106	0.001223096	0.1956522
4	-0.4958860	0.2644725	-0.68711980	0.8147933	0.191108771	0.1956522
5	-0.1052403	-0.1052403	-0.51556993	1.0659658	0.124718160	0.1739130
6	-3.0234590	4.1702883	4.62507344	4.6793342	7.627906977	0.8913043 *

6 rows

Hide

```
influence.measures(reg)$is.inf
```

```
dfb.1_ dfb.x1 dffit cov.r cook.d hat
1 FALSE FALSE FALSE FALSE FALSE FALSE
2 FALSE FALSE FALSE FALSE FALSE FALSE
3 FALSE FALSE FALSE FALSE FALSE FALSE
4 FALSE FALSE FALSE FALSE FALSE FALSE
5 FALSE FALSE FALSE FALSE FALSE FALSE
6 TRUE TRUE TRUE TRUE TRUE FALSE
```

Hide

```
lm.influence(reg)
```

```
$hat
      1      2      3      4      5      6
0.3478261 0.1956522 0.1956522 0.1956522 0.1739130 0.8913043

$coefficients
      (Intercept)      x1
1  0.67826087 -0.130434783
2  0.37015276 -0.049353702
3 -0.03525264  0.004700353
4 -0.44065805  0.058754407
5 -0.10068650 -0.025171625
6 -2.52173913  0.869565217

$sigma
      1      2      3      4      5      6
0.9660918 0.9491580 1.1150082 0.8699177 0.9365858 0.8164966

$wt.res
      1      2      3      4      5
0.78260870 0.91304348 -0.08695652 -1.08695652 -0.95652174
      6
0.43478261
```

Hide

```
summary.aov(lm(y1[-6]~x1[-6]))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
x1[-6]	1	0	0.0000	0	1
Residuals	3	2	0.6667		

## Section 9.15

## Section 9.16

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/school/statistical data management/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

[Hide](#)

```
data <- read.table("ipomopsis.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1 and only the first element will be used

[Hide](#)

```
attach(data)
names(data)
```

```
[1] "Root"    "Fruit"   "Grazing"
```

## Section 9.16.1

[Hide](#)

```
model <- lm(Fruit[Grazing=="Grazed"]~Root[Grazing=="Grazed"])
model <- lm(Fruit~Root,subset=(Grazing=="Grazed"))
```

## section 9.16.2

[Hide](#)

```
model <- lm(Fruit~Grazing,weights=Root)
summary(model)
```

Call:

```
lm(formula = Fruit ~ Grazing, weights = Root)
```

Weighted Residuals:

Min	1Q	Median	3Q	Max
-137.822	-53.551	0.381	30.259	145.132

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	70.725	4.849	14.59	<2e-16 ***
GrazingUngrazed	-16.953	7.469	-2.27	0.029 *

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 62.51 on 38 degrees of freedom

Multiple R-squared: 0.1194, Adjusted R-squared: 0.0962

F-statistic: 5.151 on 1 and 38 DF, p-value: 0.02899

[Hide](#)

```
model <- lm(Fruit~Grazing)
summary(model)
```

Call:

```
lm(formula = Fruit ~ Grazing)
```

Residuals:

Min	1Q	Median	3Q	Max
-52.991	-18.028	2.915	14.049	48.109

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	67.941	5.236	12.976	1.54e-15 ***
GrazingUngrazed	-17.060	7.404	-2.304	0.0268 *

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 23.41 on 38 degrees of freedom

Multiple R-squared: 0.1226, Adjusted R-squared: 0.09949

F-statistic: 5.309 on 1 and 38 DF, p-value: 0.02678

## Section 9.16.3

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/school/statistical data management/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
data <- read.table("ipomopsis.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

Hide

```
attach(data)
```

The following object is masked `_by_ .GlobalEnv`:

Root

The following objects are masked from data (pos = 3):

Fruit, Grazing, Root

Hide

```
names(data)
```

```
[1] "Root"    "Fruit"   "Grazing"
```

Hide

```
# 9.16.1 Subsets
```

```
model <- lm(Fruit[Grazing=="Grazed"]~Root[Grazing=="Grazed"])
```

```
model <- lm(Fruit~Root,subset=(Grazing=="Grazed"))
```

```
# 9.16.2 Weights
```

```
model <- lm(Fruit~Grazing,weights=Root)
```

```
summary(model)
```

Call:

```
lm(formula = Fruit ~ Grazing, weights = Root)
```

Weighted Residuals:

	Min	1Q	Median	3Q	Max
	-140.177	-54.293	-0.397	29.896	142.080

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	71.678	4.990	14.366	<2e-16 ***
GrazingUngrazed	-17.906	7.576	-2.364	0.0235 *

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 62.72 on 37 degrees of freedom

(1 observation deleted due to missingness)

Multiple R-squared: 0.1312, Adjusted R-squared: 0.1077

F-statistic: 5.587 on 1 and 37 DF, p-value: 0.02346

[Hide](#)

```
model <- lm(Fruit~Grazing)
summary(model)
```

Call:

```
lm(formula = Fruit ~ Grazing)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-52.991	-18.028	2.915	14.049	48.109

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	67.941	5.236	12.976	1.54e-15 ***
GrazingUngrazed	-17.060	7.404	-2.304	0.0268 *

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 23.41 on 38 degrees of freedom

Multiple R-squared: 0.1226, Adjusted R-squared: 0.09949

F-statistic: 5.309 on 1 and 38 DF, p-value: 0.02678

[Hide](#)

```
Root[37] <- NA
model <- lm(Fruit~Grazing*Root)
model <- lm(Fruit~Grazing*Root,na.action=na.fail)
```



```
Error in na.fail.default(list(Fruit = c(59.77, 60.98, 14.73, 19.28, 34.25,  :
  missing values in object
```

## Section 9.17

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

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Hide

```
data <- read.table("regression.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

Hide

```
attach(data)
names(data)
```

```
[1] "growth" "tannin"
```

Hide

```
model <- lm(growth~tannin)
n <- length(growth)
sse <- sum((growth-fitted(model))^2)
s2 <- sse/(n-2)
s <- sqrt(s2)

-(n/2)*log(2*pi)-n*log(s)-sse/(2*s2)
```

```
[1] -16.51087
```

Hide

```
logLik(model)
```

```
'log Lik.' -16.37995 (df=3)
```

Hide

```
-2 * -16.37995 + 6
```

```
[1] 38.7599
```

Hide

```
AIC(model)
```

```
[1] 38.7599
```

## Section 9.17.1

Hide

```
model.1 <- lm(Fruit~Grazing*Root)
model.2 <- lm(Fruit~Grazing+Root)
AIC(model.1, model.2)
```

	<b>df</b> <dbl>	<b>AIC</b> <dbl>
model.1	5	263.6269
model.2	4	261.7835
2 rows		

Hide

```
-2*logLik(model.1)+2*(4+1)
```

```
'log Lik.' 263.6269 (df=5)
```

Hide

```
-2*logLik(model.2)+2*(3+1)
```

```
'log Lik.' 261.7835 (df=4)
```

Hide

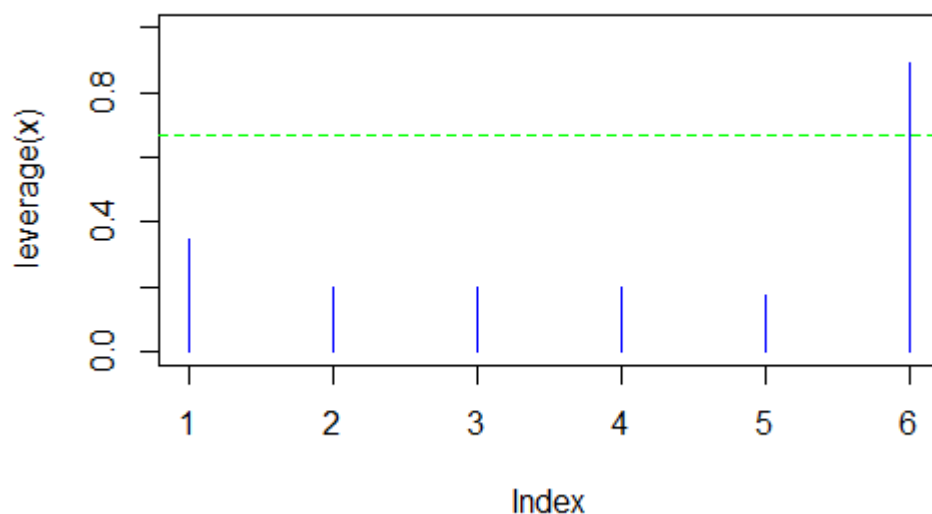
```
#models <- list (model1, model2, model3, model4, model5, model6)
models <- list (model.1, model.2)
aic <- unlist(lapply(models, AIC))
aic
```

```
[1] 263.6269 261.7835
```

# Section 9.18

Hide

```
x <- c(2,3,3,3,4,7)
leverage <- function(x){1/length(x)+(x-mean(x))^2/sum((x-mean(x))^2)}
plot(leverage(x),type="h",ylim=c(0,1),col="blue")
abline(h=4/6,lty=2,col="green")
```



## section 9.19

## Section 9.20

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/school/statistical data management/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
Decay <- read.table("Decay.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1 and only the first element will be used

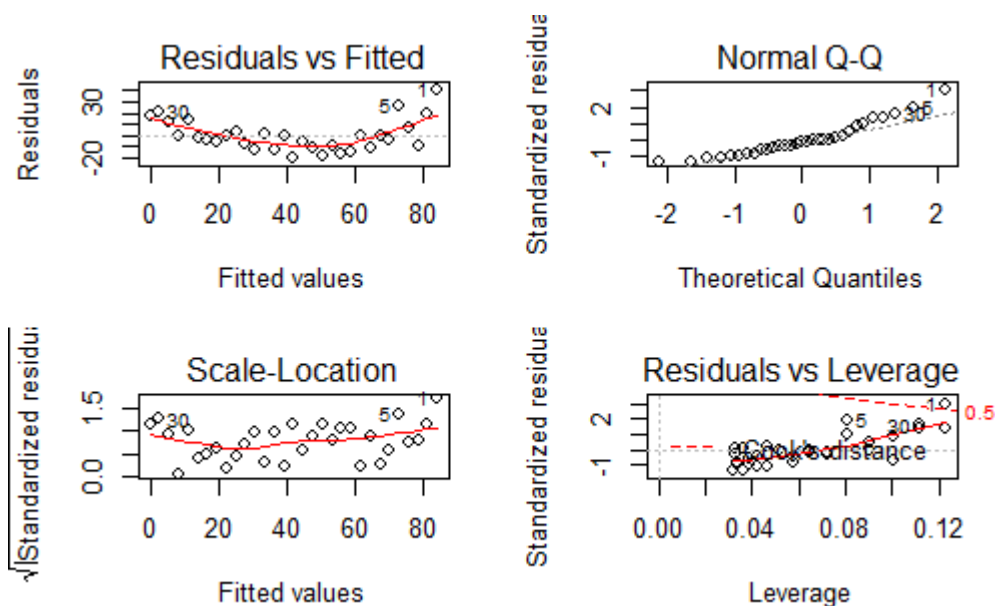
Hide

```
attach(Decay)
names(Decay)
```

```
[1] "time"    "amount"
```

Hide

```
model <- lm(amount~time)
par(mfrow=c(2,2))
plot(model)
```



## Section 9.21

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/school/statistical data management/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
data <- read.table("regression.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

Hide

```
attach(data)
```

The following objects are masked from data (pos = 4):

```
growth, tannin
```

Hide

```
names(data)
```

```
[1] "growth" "tannin"
```

Hide

```
model <- lm(growth~tannin)
summary(model)
```

Call:

```
lm(formula = growth ~ tannin)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.4556	-0.8889	-0.2389	0.9778	2.8944

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	11.7556	1.0408	11.295	9.54e-06 ***
tannin	-1.2167	0.2186	-5.565	0.000846 ***

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.693 on 7 degrees of freedom

Multiple R-squared: 0.8157, Adjusted R-squared: 0.7893

F-statistic: 30.97 on 1 and 7 DF, p-value: 0.0008461

## Section 9.21.1

Hide

```
coef(model)
```

```
(Intercept)      tannin
 11.75556      -1.21667
```

Hide

```
fitted(model)
```

	1	2	3	4	5	6
11.755556	10.538889	9.322222	8.105556	6.888889	5.672222	
	7	8	9			
4.455556	3.238889	2.022222				

Hide

```
resid(model)
```

	1	2	3	4	5
0.2444444	-0.5388889	-1.3222222	2.8944444	-0.8888889	
	6	7	8	9	
1.3277778	-2.4555556	-0.2388889	0.9777778		

Hide

```
vcov(model)
```

	(Intercept)	tannin
(Intercept)	1.083263	-0.19116402
tannin	-0.191164	0.04779101

## Section 9.21.2

Hide

```
summary.aov(model)
```

```

      Df Sum Sq Mean Sq F value    Pr(>F)
tannin   1  88.82   88.82   30.97 0.000846 ***
Residuals  7  20.07    2.87
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Hide

```
summary.aov(model)[[1]][1]
```

	Df
tannin	1
Residuals	7

Hide

```
summary.aov(model)[[1]][2]
```

	Sum Sq
tannin	88.817
Residuals	20.072

[Hide](#)

```
summary.aov(model)[[1]][3]
```

	Mean Sq
tannin	88.817
Residuals	2.867

[Hide](#)

```
summary.aov(model)[[1]][4]
```

	F value
tannin	30.974
Residuals	

[Hide](#)

```
summary.aov(model)[[1]][5]
```

	Pr(>F)
tannin	0.0008461 ***
Residuals	

---

Signif. codes:  
0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

[Hide](#)

```
as.numeric(unlist(summary.aov(model)[[1]][4]))[1]
```

```
[1] 30.97398
```

[Hide](#)

```
summary(model)
```

Call:

```
lm(formula = growth ~ tannin)
```

Residuals:

Min	1Q	Median	3Q	Max
-2.4556	-0.8889	-0.2389	0.9778	2.8944

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	11.7556	1.0408	11.295	9.54e-06 ***
tannin	-1.2167	0.2186	-5.565	0.000846 ***

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.693 on 7 degrees of freedom

Multiple R-squared: 0.8157, Adjusted R-squared: 0.7893

F-statistic: 30.97 on 1 and 7 DF, p-value: 0.0008461

[Hide](#)

```
summary(model)[[1]]
```

```
lm(formula = growth ~ tannin)
```

[Hide](#)

```
summary(model)[[2]]
```



```

growth ~ tannin
attr("variables")
list(growth, tannin)
attr("factors")
  tannin
growth      0
tannin      1
attr("term.labels")
[1] "tannin"
attr("order")
[1] 1
attr("intercept")
[1] 1
attr("response")
[1] 1
attr("Environment")
<environment: R_GlobalEnv>
attr("predvars")
list(growth, tannin)
attr("dataClasses")
  growth  tannin
"numeric" "numeric"

```

Hide

```
summary(model)[[3]]
```

1	2	3	4	5
0.2444444	-0.5388889	-1.3222222	2.8944444	-0.8888889
6	7	8	9	
1.3277778	-2.4555556	-0.2388889	0.9777778	

Hide

```
summary(model)[[4]]
```

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	11.755556	1.0407991	11.294740	9.537315e-06
tannin	-1.216667	0.2186115	-5.565427	8.460738e-04

Hide

```
summary(model)[[4]] [1]
```

```
[1] 11.75556
```

Hide

```
summary(model)[[4]] [2]
```

```
[1] -1.216667
```

[Hide](#)

```
summary(model)[[4]] [3]
```

```
[1] 1.040799
```

[Hide](#)

```
summary(model)[[4]] [4]
```

```
[1] 0.2186115
```

[Hide](#)

```
summary(model)[[4]] [8]
```

```
[1] 0.0008460738
```

[Hide](#)

```
summary(model)[[5]]
```

```
(Intercept)      tannin  
      FALSE      FALSE
```

[Hide](#)

```
summary(model)[[6]]
```

```
[1] 1.693358
```

[Hide](#)

```
summary(model)[[7]]
```

```
[1] 2 7 2
```

[Hide](#)

```
summary(model)[[8]]
```

```
[1] 0.8156633
```

[Hide](#)

```
summary(model)[[9]]
```

```
[1] 0.7893294
```

Hide

```
summary(model)[[10]]
```

value	numdf	dendf
30.97398	1.00000	7.00000

Hide

```
summary(model)[[11]]
```

	(Intercept)	tannin
(Intercept)	0.37777778	-0.06666667
tannin	-0.06666667	0.01666667

## Section 9.21.3

Hide

```
model$coef
```

	(Intercept)	tannin
	11.755556	-1.216667

Hide

```
model$df
```

```
[1] 7
```

## Section 9.21.4

Hide

```
x <- 0:100
y <- 17+0.2*x+3*rnorm(101)
model0 <- lm(y~1)
model1 <- lm(y~x)
model2 <- lm(y~x+I(x^2))
models <- list(model0,model1,model2)
lapply(models,coef)
```

```
[[1]]
(Intercept)
  27.27264

[[2]]
(Intercept)          x
 16.7263447    0.2109259

[[3]]
(Intercept)          x      I(x^2)
16.4514690236    0.2275850298 -0.0001665913
```

Hide

```
as.vector(unlist(lapply(models,coef)))[c(1,2,4)]
```

```
[1] 27.27264 16.72634 16.45147
```

Hide

```
lapply(models,AIC)
```

```
[[1]]
[1] 676.351

[[2]]
[1] 499.3803

[[3]]
[1] 501.171
```

## Section 9.22

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/school/statistical data management/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
comp <- read.table("competition.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

Hide

```
attach(comp)
names(comp)
```

```
[1] "biomass" "clipping"
```

Hide

```
levels(clipping)
```

```
[1] "control" "n25"      "n50"      "r10"      "r5"
```

Hide

```
# The analysis of variance model is fitted like this:
model <- lm(biomass~clipping)
summary.aov(model)
```

```
           Df Sum Sq Mean Sq F value   Pr(>F)
clipping    4  85356    21339   4.302 0.00875 **
Residuals   25 124020     4961
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hide

```
summary.lm(model)
```

```
Call:
lm(formula = biomass ~ clipping)

Residuals:
    Min       1Q   Median       3Q      Max
-103.333  -49.667    3.417   43.375  177.667

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   465.17     28.75   16.177  9.4e-15 ***
clippingn25    88.17     40.66    2.168  0.03987 *
clippingn50   104.17     40.66    2.562  0.01683 *
clippingr10   145.50     40.66    3.578  0.00145 **
clippingr5    145.33     40.66    3.574  0.00147 **
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.43 on 25 degrees of freedom
Multiple R-squared:  0.4077,    Adjusted R-squared:  0.3129
F-statistic: 4.302 on 4 and 25 DF,  p-value: 0.008752
```

Hide

```
comp[1,]
```

biomass clipping	
	<div>&lt;int&gt; &lt;fctr&gt;</div>
1	551 n25
1 row	

Hide

```
means <- tapply(biomass,clipping,mean)
means
```

control	n25	n50	r10	r5
465.1667	553.3333	569.3333	610.6667	610.5000

Hide

```
means[2]-means[1]
```

n25
88.16667

Hide

```
means[3]-means[1]
```

```
      n50  
104.1667
```

Hide

```
means[4]-means[1]
```

```
      r10  
145.5
```

Hide

```
means[5]-means[1]
```

```
      r5  
145.3333
```

Hide

```
sqrt(4961/6)
```

```
[1] 28.75471
```

Hide

```
sqrt(2*4961/6)
```

```
[1] 40.6653
```

## Section 9.23

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/school/statistical data management/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
comp <- read.table("competition.txt",header=T)
```

the condition has length > 1 and only the first element will be usedthe condition has length > 1 and only the first element will be used

[Hide](#)

```
attach(comp)
```

The following objects are masked from comp (pos = 3):

biomass, clipping

[Hide](#)

```
names(comp)
```

```
[1] "biomass" "clipping"
```

[Hide](#)

```
model1 <- aov(biomass~clipping)
summary(model1)
```

```
              Df Sum Sq Mean Sq F value    Pr(>F)
clipping         4  85356    21339   4.302 0.00875 **
Residuals       25 124020     4961
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

[Hide](#)

```
summary.lm(model1)
```



Call:

```
aov(formula = biomass ~ clipping)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-103.333	-49.667	3.417	43.375	177.667

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	465.17	28.75	16.177	9.4e-15	***
clippingn25	88.17	40.66	2.168	0.03987	*
clippingn50	104.17	40.66	2.562	0.01683	*
clippingr10	145.50	40.66	3.578	0.00145	**
clippingr5	145.33	40.66	3.574	0.00147	**

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.43 on 25 degrees of freedom

Multiple R-squared: 0.4077, Adjusted R-squared: 0.3129

F-statistic: 4.302 on 4 and 25 DF, p-value: 0.008752

[Hide](#)

```
levels(clipping)
```

```
[1] "control" "n25"      "n50"      "r10"      "r5"
```

## Section 9.23.3

[Hide](#)

```
contrasts(clipping) <-  
  cbind(c(4, -1, -1, -1, -1), c(0, 1, 1, -1, -1), c(0, 0, 0, 1, -1), c(0, 1, -1, 0, 0))
```

```
clipping
```

```

[1] n25      n25      n25      n25      n25      n25      n50
[8] n50      n50      n50      n50      n50      r5       r5
[15] r5       r5       r5       r5       control control control
[22] control control control r10      r10      r10      r10
[29] r10      r10
attr(,"contrasts")
      [,1] [,2] [,3] [,4]
control    4    0    0    0
n25        -1    1    0    1
n50        -1    1    0   -1
r10        -1   -1    1    0
r5         -1   -1   -1    0
Levels: control n25 n50 r10 r5

```

Hide

```

model2 <- aov(biomass~clipping)
summary.lm(model2)

```

```

Call:
aov(formula = biomass ~ clipping)

Residuals:
    Min       1Q   Median       3Q      Max
-103.333  -49.667    3.417   43.375  177.667

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  561.80000   12.85926  43.688 < 2e-16 ***
clipping1    -24.15833    6.42963  -3.757 0.000921 ***
clipping2    -24.62500   14.37708  -1.713 0.099128 .
clipping3     0.08333   20.33227   0.004 0.996762
clipping4    -8.00000   20.33227  -0.393 0.697313
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.43 on 25 degrees of freedom
Multiple R-squared:  0.4077,    Adjusted R-squared:  0.3129
F-statistic: 4.302 on 4 and 25 DF,  p-value: 0.008752

```

Hide

```
mean(biomass)
```

```
[1] 561.8
```

Hide

```
tapply(biomass,clipping,mean)
```

```
control      n25      n50      r10      r5
465.1667 553.3333 569.3333 610.6667 610.5000
```

Hide

```
c1 <- factor(1+(clipping!="control"))
tapply(biomass,c1,mean)
```

```
      1      2
465.1667 585.9583
```

Hide

```
mean(biomass) - tapply(biomass,c1,mean)[2]
```

```
      2
-24.15833
```

Hide

```
c2 <- factor(2*(clipping=="n25")+2*(clipping=="n50")+
             (clipping=="r10")+(clipping=="r5"))
(tapply(biomass,c2,mean)[3]- tapply(biomass,c2,mean)[2])/2
```

```
      2
-24.625
```

Hide

```
(610.666666-610.5)/2
```

```
[1] 0.083333
```

Hide

```
(553.3333-569.3333)/2
```

```
[1] -8
```

Hide

```
sqrt(4961/(5*4*6))
```

```
[1] 6.429749
```

Hide

```
sqrt(2*(4961/12))/2
```

```
[1] 14.37735
```

Hide

```
sqrt(2*(4961/6))/2
```

```
[1] 20.33265
```

## Section 9.24

Hide

```
contrasts(clipping) <- NULL
options(contrasts=c("contr.treatment","contr.poly"))

model3 <- aov(biomass~clipping)
summary.lm(model3)
```

Call:  
aov(formula = biomass ~ clipping)

Residuals:

Min	1Q	Median	3Q	Max
-103.333	-49.667	3.417	43.375	177.667

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	465.17	28.75	16.177	9.4e-15	***
clippingn25	88.17	40.66	2.168	0.03987	*
clippingn50	104.17	40.66	2.562	0.01683	*
clippingr10	145.50	40.66	3.578	0.00145	**
clippingr5	145.33	40.66	3.574	0.00147	**

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.43 on 25 degrees of freedom

Multiple R-squared: 0.4077, Adjusted R-squared: 0.3129

F-statistic: 4.302 on 4 and 25 DF, p-value: 0.008752

Hide

```
clip2 <- clipping
levels(clip2)
```

```
[1] "control" "n25"      "n50"      "r10"      "r5"
```

Hide

```
levels(clip2)[4:5] <- "root"
```

```
model4 <- aov(biomass~clip2)
anova(model3,model4)
```

#### Analysis of Variance Table

Model 1: biomass ~ clipping

Model 2: biomass ~ clip2

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	25	124020				
2	26	124020	-1	-0.083333	0	0.9968

Hide

```
summary.lm(model4)
```

Call:

```
aov(formula = biomass ~ clip2)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-103.333	-49.667	3.417	43.417	177.667

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	465.17	28.20	16.498	2.72e-15 ***
clip2n25	88.17	39.87	2.211	0.036029 *
clip2n50	104.17	39.87	2.612	0.014744 *
clip2root	145.42	34.53	4.211	0.000269 ***

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 69.07 on 26 degrees of freedom

Multiple R-squared: 0.4077, Adjusted R-squared: 0.3393

F-statistic: 5.965 on 3 and 26 DF, p-value: 0.003099

Hide

```
clip3 <- clip2
levels(clip3)[2:3] <- "shoot"
levels(clip3)
```

```
[1] "control" "shoot"   "root"
```

Hide

```
model5 <- aov(biomass~clip3)
anova(model4,model5)
```

#### Analysis of Variance Table

Model 1: biomass ~ clip2

Model 2: biomass ~ clip3

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	26	124020				
2	27	124788	-1	-768	0.161	0.6915

Hide

```
clip4 <- clip3
levels(clip4)[2:3] <- "pruned"
levels(clip4)
```

```
[1] "control" "pruned"
```

Hide

```
model6 <- aov(biomass~clip4)
anova(model5,model6)
```

#### Analysis of Variance Table

Model 1: biomass ~ clip3

Model 2: biomass ~ clip4

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	27	124788				
2	28	139342	-1	-14553	3.1489	0.08726 .

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Hide

```
summary.lm(model6)
```

```
Call:
aov(formula = biomass ~ clip4)

Residuals:
    Min       1Q   Median       3Q      Max
-135.958  -49.667   -4.458   50.635  145.042

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    465.2      28.8    16.152 1.01e-15 ***
clip4pruned    120.8      32.2     3.751 0.000815 ***
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.54 on 28 degrees of freedom
Multiple R-squared:  0.3345,    Adjusted R-squared:  0.3107
F-statistic: 14.07 on 1 and 28 DF,  p-value: 0.0008149
```

Hide

```
tapply(biomass,clip4,mean)
```

```
control  pruned
465.1667 585.9583
```

Hide

```
model7 <- aov(biomass~1)
anova(model6,model7)
```

#### Analysis of Variance Table

```
Model 1: biomass ~ clip4
Model 2: biomass ~ 1
  Res.Df    RSS Df Sum of Sq    F    Pr(>F)
1      28 139342
2      29 209377 -1    -70035 14.073 0.0008149 ***
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Section 9.25

### Section 9.25.1

Hide

```
options(contrasts=c("contr.treatment","contr.poly"))
contrasts(clipping)
```

```
      n25 n50 r10 r5
control  0  0  0  0
n25      1  0  0  0
n50      0  1  0  0
r10      0  0  1  0
r5       0  0  0  1
```

Hide

```
output.treatment <- lm(biomass~clipping)
summary(output.treatment)
```

```
Call:
lm(formula = biomass ~ clipping)

Residuals:
    Min       1Q   Median       3Q      Max
-103.333  -49.667   3.417  43.375  177.667

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   465.17     28.75  16.177  9.4e-15 ***
clippingn25    88.17     40.66   2.168  0.03987 *
clippingn50   104.17     40.66   2.562  0.01683 *
clippingr10   145.50     40.66   3.578  0.00145 **
clippingr5    145.33     40.66   3.574  0.00147 **
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.43 on 25 degrees of freedom
Multiple R-squared:  0.4077,    Adjusted R-squared:  0.3129
F-statistic: 4.302 on 4 and 25 DF,  p-value: 0.008752
```

## Section 9.25.2

Hide

```
options(contrasts=c("contr.helmert","contr.poly"))
contrasts(clipping)
```



	[,1]	[,2]	[,3]	[,4]
control	-1	-1	-1	-1
n25	1	-1	-1	-1
n50	0	2	-1	-1
r10	0	0	3	-1
r5	0	0	0	4

Hide

```
output.helmert <- lm(biomass~clipping)
summary(output.helmert)
```

Call:

```
lm(formula = biomass ~ clipping)
```

Residuals:

Min	1Q	Median	3Q	Max
-103.333	-49.667	3.417	43.375	177.667

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	561.800	12.859	43.688	<2e-16 ***
clipping1	44.083	20.332	2.168	0.0399 *
clipping2	20.028	11.739	1.706	0.1004
clipping3	20.347	8.301	2.451	0.0216 *
clipping4	12.175	6.430	1.894	0.0699 .

---

Signif. codes:

0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.43 on 25 degrees of freedom

Multiple R-squared: 0.4077, Adjusted R-squared: 0.3129

F-statistic: 4.302 on 4 and 25 DF, p-value: 0.008752

Hide

$$(465.16667+553.33333)/2-465.16667$$

```
[1] 44.08333
```

Hide

$$(465.16667+553.33333+569.33333)/3-(465.16667+553.33333)/2$$

```
[1] 20.02779
```

Hide

$$(465.16667+553.33333+569.33333+610.66667)/4-(553.33333+465.16667+569.33333)/3$$

```
[1] 20.34725
```

Hide

```
mean(biomass)-(465.16667+553.33333+569.333333+610.66667)/4
```

```
[1] 12.175
```

Hide

```
sqrt(4961/30)
```

```
[1] 12.8595
```

Hide

```
sqrt(4961/(2*6))
```

```
[1] 20.33265
```

Hide

```
sqrt(4961/(3*2*6))
```

```
[1] 11.73906
```

Hide

```
sqrt(4961/(4*3*6))
```

```
[1] 8.30077
```

Hide

```
sqrt(4961/(5*4*6))
```

```
[1] 6.429749
```

## Section 9.25.3

Hide

```
options(contrasts=c("contr.sum","contr.poly"))  
output.sum <- lm(biomass~clipping)  
summary(output.sum)
```

```
Call:
lm(formula = biomass ~ clipping)

Residuals:
    Min       1Q   Median       3Q      Max
-103.333  -49.667    3.417   43.375  177.667

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  561.800     12.859   43.688 < 2e-16 ***
clipping1    -96.633     25.719   -3.757 0.000921 ***
clipping2     -8.467     25.719   -0.329 0.744743
clipping3      7.533     25.719    0.293 0.772005
clipping4     48.867     25.719    1.900 0.069019 .
---
Signif. codes:
  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 70.43 on 25 degrees of freedom
Multiple R-squared:  0.4077,    Adjusted R-squared:  0.3129
F-statistic: 4.302 on 4 and 25 DF,  p-value: 0.008752
```

Hide

```
tapply(biomass,clipping,mean) - 561.8
```

```
control      n25      n50      r10      r5
-96.633333  -8.466667   7.533333  48.866667  48.700000
```

Hide

```
sqrt(4961/30+4961/10)
```

```
[1] 25.71899
```

## Section 9.26

## Section 9.27

Hide

```
setwd("C:/Users/Nathan/Desktop/school/statistical data management/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/school/statistical data management/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
data <- read.table("poly.txt",header=T)
```

the condition has length > 1 and only the first element will be used  
the condition has length > 1  
and only the first element will be used

Hide

```
attach(data)
names(data)
```

```
[1] "treatment" "response"
```

Hide

```
tapply(response,treatment,mean)
```

```
high    low medium    none
4.50    5.25   7.00    2.50
```

Hide

```
summary.aov(model)
```

```
          Df Sum Sq Mean Sq F value    Pr(>F)
clipping    4  85356    21339   4.302 0.00875 **
Residuals   25 124020     4961
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hide

```
is.factor(treatment)
```

```
[1] TRUE
```

Hide

```
is.ordered(treatment)
```

```
[1] FALSE
```

Hide

```
treatment <- ordered(treatment,levels=c("none","low","medium","high"))
levels(treatment)
```

```
[1] "none"    "low"     "medium"  "high"
```

Hide

```
model2 <- lm(response~treatment)
summary.aov(model2)
```

```
          Df Sum Sq Mean Sq F value    Pr(>F)
treatment   3  41.69  13.896    24.7 2.02e-05 ***
Residuals  12   6.75   0.563
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Hide

```
summary.lm(model2)
```

```
Call:
lm(formula = response ~ treatment)
```

```
Residuals:
```

```
    Min       1Q   Median       3Q      Max
-1.25  -0.50   0.00   0.50   1.00
```

```
Coefficients:
```

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   4.8125     0.1875  25.667 7.45e-12 ***
treatment.L    1.7330     0.3750   4.621 0.000589 ***
treatment.Q   -2.6250     0.3750  -7.000 1.43e-05 ***
treatment.C   -0.7267     0.3750  -1.938 0.076520 .
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Residual standard error: 0.75 on 12 degrees of freedom
Multiple R-squared:  0.8606,    Adjusted R-squared:  0.8258
F-statistic: 24.7 on 3 and 12 DF,  p-value: 2.015e-05
```

Hide

```
tapply(response,treatment,mean)
```

```
none    low medium    high
2.50    5.25   7.00    4.50
```

Hide

```
yv <- as.vector(tapply(response,treatment,mean))
x <- 1:4
model <- lm(yv~x+I(x^2)+I(x^3))
summary(model)
```

Call:

```
lm(formula = yv ~ x + I(x^2) + I(x^3))
```

Residuals:

ALL 4 residuals are 0: no residual degrees of freedom!

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.0000	NA	NA	NA
x	-1.7083	NA	NA	NA
I(x^2)	2.7500	NA	NA	NA
I(x^3)	-0.5417	NA	NA	NA

Residual standard error: NaN on 0 degrees of freedom

Multiple R-squared: 1, Adjusted R-squared: NaN

F-statistic: NaN on 3 and 0 DF, p-value: NA

[Hide](#)

```
x <- 1:4
x2 <- x^2
x3 <- x^3
cor(cbind(x,x2,x3))
```

	x	x2	x3
x	1.0000000	0.9843740	0.9513699
x2	0.9843740	1.0000000	0.9905329
x3	0.9513699	0.9905329	1.0000000

[Hide](#)

```
t(contrasts(treatment))
```

	[,1]	[,2]	[,3]	[,4]
.L	-0.6708204	-0.2236068	0.2236068	0.6708204
.Q	0.5000000	-0.5000000	-0.5000000	0.5000000
.C	-0.2236068	0.6708204	-0.6708204	0.2236068

[Hide](#)

```
4.8125 - 0.6708204*1.733 - 0.5*2.6250 + 0.2236068*0.7267
```

```
[1] 2.499963
```

Hide

```
4.8125 - 0.2236068*1.733+0.5*2.6250 - 0.6708204*0.7267
```

```
[1] 5.250004
```

Hide

```
4.8125 + 0.2236068*1.733 + 0.5*2.6250 + 0.6708204*0.7267
```

```
[1] 6.999996
```

Hide

```
4.8125 + 0.6708204*1.733 - 0.5*2.6250 - 0.2236068*0.7267
```

```
[1] 4.500037
```

Hide

```
y <- as.vector(tapply(response,treatment,mean))
model <- lm(y~poly(x,3))
summary(model)
```

Call:

```
lm(formula = y ~ poly(x, 3))
```

Residuals:

ALL 4 residuals are 0: no residual degrees of freedom!

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	4.8125	NA	NA	NA
poly(x, 3)1	1.7330	NA	NA	NA
poly(x, 3)2	-2.6250	NA	NA	NA
poly(x, 3)3	-0.7267	NA	NA	NA

Residual standard error: NaN on 0 degrees of freedom

Multiple R-squared: 1, Adjusted R-squared: NaN

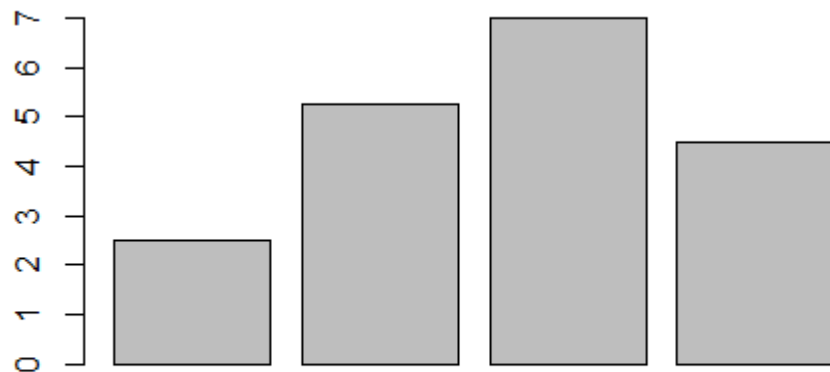
F-statistic: NaN on 3 and 0 DF, p-value: NA

Hide

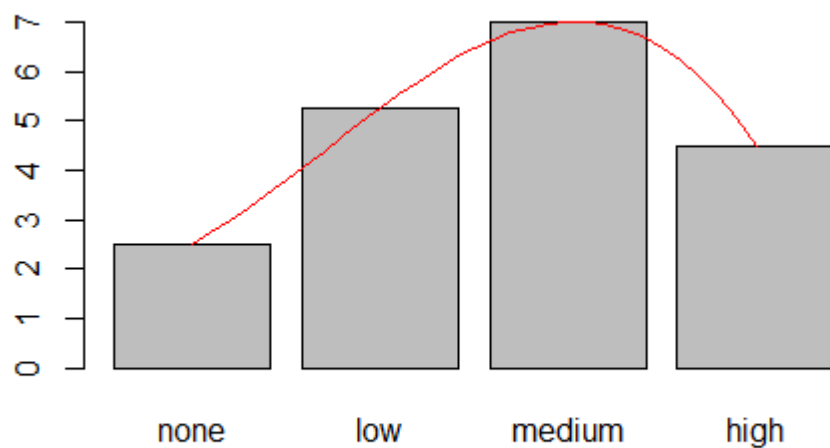
```
xv <- seq(1,4,0.1)
yv <- predict(model,list(x=xv))

(bar.x <- barplot(y))
```

```
[,1]  
[1,] 0.7  
[2,] 1.9  
[3,] 3.1  
[4,] 4.3
```

[Hide](#)

```
barplot(y, names=levels(treatment))  
xs <- -0.5 + 1.2 * xv  
lines(xs, yv, col="red")
```



END OF CODE